

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Portugal, Frank H.
Colwell, Rita R.
Hug, Anwarul
Chowdhury, Afzal

(ii) TITLE OF INVENTION: Compositions and Methods for
Differentiating Among *Shigella* Species
and *Shigella* from *E. coli* Species

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: 816 Congress Avenue, Suite 1900
(C) CITY: Austin
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 78701

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not Yet Assigned
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Not Yet Assigned

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,117
(B) FILING DATE: 20-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Norberg, Gloria L.
(B) REGISTRATION NUMBER: 36,706
(C) REFERENCE/DOCKET NUMBER: 044198.0000

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (512) 499-6200
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAGTTTGAT CATGGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACGGTTACCT TGTTACGACT T 21

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGGGCAGGC CTAACACATG CAAGTCGAAC 60
GGTAACAGGA AGCAGCTTGC TGTTCGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG 120
GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG 180
CAAGACCAAA GAGGGGGACC TTCGGGCCTC TTGCCATCGG ATGTGCCCAG ATGGGATTAG 240
CTAGTAGGTG GGGTAACGGC TCACCTAGGC GACGATCCCT AGCTGGTCTG AGAGGATGAC 300
CAGCCACACT GGAAC TGAGA CACGGTCCAG ACTCCTACGG GAGGCAGCAG TGGGGAATAT 360
TGCACAATGG GCGCAAGCCT GATGCAGCCA TGCCGCGTGT ATGAAGAAGG CCTTCGGGTT 420
GTAAAGTACT TTCAGCGGGG AGGAAGGGAG TAAAGTTAAT ACCTTTGCTC ATTGACGTTA 480
CCCGCAGAAG AAGCACC GGC TAACCCGTG CCAGCAGCCG CGGTAATACG GAGGGTGCAA 540
GCGTTAATCG GAATTACTGG GCGTAAAGCG CACGCAGGCG GTTTGTTAAG TCAGATGTGA 600
AATCCCCGGG CTCAACCTGG GAACTGCATC TGATACTGGC AAGCTTGAGT CTCGTAGAGG 660
GGGGTAGAAT TCCAGGTGTA GCGGTGAAAT GCGTAAAGAT CTGGAGGAAT ACCGGTGGCG 720
AAGGCGGCCC CTTGGACGAA GACTGACGCT CAGGTGCGAA AGCGTGGGGA GCAAACAGGA 780
TTAGATACCC TGGTAGTCCA CGCTGTAAAC GATGTCGACT TGGAGGTTGT GCCCTTGAGG 840
TGTGGCTTCC GGAGCTAACG CGTTAAGTCG ACCGCCTGGG GAGTACGGCC GCAAGGTTAA 900
AACTCAAATG AATTGACGGG GGCCCGCACA AGCGGTGGAG CATGTGGTTT AATTGATGC 960
AACGCGAAGA ACCTTACCTG GTCTTGACAT CCACGGAAGT TTTCAGAGAT GAGAATGTGC 1020
CTTCGGGAAC CGTGAGACAG GTGCTGCATG GCTGTCGTCA GCTCGTGTG TGAAATGTTG 1080
GGTTAAGTCC CGCAACGAGC GCAACCCTTA TCCTTTGTTG CCAGCGGTCC GGCCGGGAAC 1140
TCAAAGGAGA CTGCCAGTGA TAACTGGAG GAAGGTGGGG ATGACGTCAA GTCATCATGG 1200
CCCTTACGAC CAGGGCTACA CACGTGCTAC AATGGCGCAT ACAAAGAGAA GCGACCTCGC 1260

GAGAGCAAGC GGACCTCATA AAGTGCGTCG TAGTCCGGAT TGGAGTCTGC AACTCGACTC 1320
 CATGAAGTCG GAATCGCTAG TAATCGTGGA TCAGAATGCC ACGGTGAATA CGTTCCCGGG 1380
 5 CCTTGACAC ACCGCCCCGTC ACACCATGGG AGTGGGTTGC AAAAGAAGTA GGTAGCTTAA 1440
 CCTTCGGGAG GGCCTTACC ACTTTGTGAT TCATGACTGG GGTGAAGTCG TAACAAGGTA 1500
 10 ACCGTA 1506

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGGCAGGC CTAACACATG CAAGTCGAAC 60
 GGTAACAGGA AACAGCTTGC TGTTCGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG 120
 25 GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG 180
 CAAGACCAAA GAGGGGGACC TTCGGGCCTC TTGCCATCGG ATGTGCCCAG ATGGGATTAG 240
 30 CTAGTAGGTG GGGTAACGGC TCACCTAGGC GACGATCCCT AGCTGGTCTG AGAGGATGAC 300
 CAGCCACACT GGAACGTAGA CACGGTCCAG ACTCCTACGG GAGGCAGCAG TGGGGAATAT 360
 TGCACAATGG GCGCAAGCCT GATGCAGCCA TGCCGCGTGT ATGAAGAAGG CCTTCGGGTT 420
 35 GTAAAGTACT TTCAGCGGGG AGGAAGGGAG TAAAGTTAAT ACCTTTACTC ATTGACGTTA 480
 CCCGCAGAAG AAGCACCGGC TAACTCCGTG CCAGCAGCCG CGGTAATACG GAGGGTGCAA 540
 40 GCGTTAATCG GAATTACTGG GCGTAAAGCG CACGCAGGCG GTTTGTTAAG TCAGATGTGA 600
 AATCCCCGGG CTCAACCTGG GAACTGCATC TGATACTGGC AAGCTTGAGT CTCGTAGAGG 660
 GGGGTAGAAT TCCAGGTGTA GCGGTGAAAT GCGTAGAGAT CTGGAGGAAT ACCGGTGGCG 720
 45 AAGGCGGCCC CCTGGACGAA GACTGACGCT CAGGTGCGAA AGCGTGGGGA GCAAACAGGA 780
 TTAGATACCC TGGTAGTCCA CGCCGTAAAC GATGTCGACT TGGAGGTTGT GCCCTTGAGG 840
 50 CGTGGCTTCC GGAGCTAACG CGTTAAGTCG ACCGCCTGGG GAGTACGGCC GCAAGGTTAA 900
 AACTCAAATG AATTGACGGG GGCCCGCACA AGCGGTGGAG CATGTGGTTT AATTCGACGC 960
 55 AACGCGAAGA ACTTACCTGG TCCTGACATC CACGGAACCT TCCAGAGATG GATTGGTGCC 1020
 TTCGGGAAC TGTGAGACAG TGCTGCATGG CTGTCGTCAG CTCGTGTTGT GAAATGTTGG 1080
 GTTAAGTCCC GCAACGAGCG CAACCCTTAT CCTTTGTTGC CAGCGGTCCG GCCGGGAAC 1140
 60 CAAAGGAGAC TGCCAGTGAT AAACCTGGAGG AAGGTGGGGA TGACGTCAAG TCATCATGGC 1200
 CCTTACGACC AGGGCTACAC ACGTGCTACA ATGGCGCATA CAAAGAGAAG CGACCTCGCG 1260
 65 AGAGCAAGCG GACCTCATAA AGTGCGTCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC 1320

	ATGAAGTCGG AATCGCTAGT AATCGTGGAT CAGAATGCCA CGGTGAATAC GTTCCCGGGC	1380
	CTTGTAACACA CCGCCCGTCA CACCATGGGA GTGGGTTGCA AAAGAAGTAG GTAGCTTAAC	1440
5	CTTCGGGAGG GCGCTTACCA CTTTGTGATT CATGACTGGG GTGAAGTCGT AACAAGGTAA	1500
	CCGTA	1505

10 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: modified_base
 (B) LOCATION: one-of(400, 593, 642, 737, 968, 998)
 (D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = Unknown"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25	AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGGCGCAGGC CTAACACATG CAAGTCGAAC	60
	GGTAACAGAA AGCAGCTTGC TCCTTTGCTG ACGAGTGGCG GACGGGTGAG TAATGTCTGG	120
30	GAAACTGCCT GATGGAGGGG GATAACTACT GGAAACGGTA GCTAATACCG CATAACGTCG	180
	CAAGACCAAA GAGGGGGACC TTCGGGCCTC TTGCCATCGG ATGTGCCCAG ATGGGATTAG	240
	CTAGTAGTGG GGTAACGGCT CACCTAGGCG ACGATCCCTA GCTGGTCTGA GAGGATGACC	300
35	AGCCCACTG GAACTGAGAC ACGGTCCAGA CTCCTACGGG AGGCAGCAGT GGGGAATATT	360
	GCACAAATGGG CGCAAGCCTG ATGCAGCCAT GCCGCGTGTN TGAANAAGGC CTTCCGGGTTG	420
40	TAAAGTACTT TCAGCGGGGA GGAAGGGAGT AAAGTTAATA CCTTTGCTCA TTGACGTTAC	480
	CCGCAGAAGA AGCACCGGCT AACTCCGTGC CAGCAGCCGC GGTAATACGG AGGGTGCAAG	540
45	CGTTAATCGG AATTACTGGG CGTAAAGCGC ACGCAGGCGG TTTGTTAAAT CANATGTGAA	600
	ATCCCCGGGC TCAACCTGGG AACTGCATCT GATACTGGCA ANCTTGAGTC TCGTAGAGGG	660
	GGGTAGAATT CCAGGTGTAG CGGTGAAATG CGTAGAGATC TGGAGGAATA CCGGTGGCGA	720
50	AGGCGGCCCC CTGGACNAAG ACTGACGCTC AGGTGCGAAA GCGTGGGGAG CAAACAGGAT	780
	TAGATACCCT GGTAGTCCAC GCCGTAAACG ATGTCGACTT GGAGGTGTGT CCCTTGAGGC	840
55	GTGGCTTCCG GAGCTAACGC GTTAAGTCGA CCGCCTGGGG AGTACGGCCG CAAGGTTAAA	900
	ACTCAAATGA ATTGACGGGG GCCCGCACAA GCGGTGGAGC ATGTGGTTTA ATTCGATGCA	960
	ACGCGAANAA CCTTACCTGG TCTTGACATC CACAGAANCT TCCAGAGATG GATTGGTGCC	1020
60	TTCCGGGAAT GTGAGACAGG TGCTGCATGG CTGTCGTCAG CTCGTGTTGT GAAATGTTGG	1080
	GTTAAGTCCC GCAACGAGCG CAACCCCTAT CCTTTGTTGC CAGCGGTCCG GCCGGGAAT	1140
65	CAAAGGAGAC TGCCAGTGAT AAAGTGGAGG AAGGTGGGGA TGACGTCAAG TCATCATGGC	1200

CCTTACGACC AGGGCTACAC ACGTGCTACA ATGGCGCATA CAAAGAGAAG CGACCTCGCG 1260
 AGAGCAAGCG GACCTCATAA AGTGCCTCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC 1320
 5 ATGAAGTCGG AATCGCTAGT AATCGTGGAT CAGAATGTCA CCGTGAATAC GTTCCCGGGC 1380
 CTTGTACACA CCGCCCGTCA CACCATGGGA GTGGCTTAAC CTTCCGGGAGG GCGCTTACCA 1440
 10 CTTTGTGATT CAT 1453

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGAGTTTGAT CATGGCTCAG ATTGAACGCT GCGGCGAGGC CTAACACATG CAAGTCGAAC 60
 GGTAACAGGA AGCAGCTTGC TCTTCGCTGA CGAGTGGCGG ACGGGTGAGT AATGTCTGGG 120
 25 AAACGCTCTG ATGGAGGGGG ATAACCTACTG GAAACGGTAG CTAATACCGC ATAATGTCCG 180
 AAGACCAAAG AGGGGGACCT TCGGGCCTCT TGCCATCGGA TGTGCCCAGA TGGGATTAGC 240
 30 TTGTTGGTGG GGTAACGGCT CACCAAGGCG ACGATCCCTA GCTGGTCTGA GAGGATGACC 300
 AGCCACATGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTG GGAATATTG 360
 CACAATGGGC GCAAGCCTGA TGCAGCCATG CCGCGTGTAT GAAGAAGGCC TTCGGGTTGT 420
 35 AAAGTACTTT CAGCGGGGAG GAAGGGAGTA AAGTTAATAC CTTTGCTCAT TGACGTTACC 480
 CGCAGAAGAA GCACCGGCTA ACTCCGTGCC AGCAGCCGCG GTAATACGGA GGGTGCAAGC 540
 40 GTTAATCGGA ATTACTGGGC GTAAAGCGCA CGCAGGCGGT TTGTTAAGTC AGATGTGAAA 600
 TCCCCGGGCT CAACCTGGGA ACTGCATCTG ATACTGGCAA GCTTGAGTCT CGTAGAGGGG 660
 45 GGTAAGAATC CAGGTGTAGC GGTGAAATGC GTAGAGATCT GGAGGAATAC CCGTGGCGAA 720
 GGCGGCCCCC TGGACGAAGA CTGACGCTCA GGTGCGAAAAG CGTGGGGAGC AAACAGGATT 780
 AGATAACCTG GTAGTCCACG CCGTAAACGA TGTCGACTTG GAGGTTGTGC CCTTGAGGCG 840
 50 TGGCTTCCGG AGCTAACGCG TTAAGTCGAC CGCCTGGGGA GTACGGCCGC AAGGTTAAAA 900
 CTCAAATGAA TTGACGGGGG CCCGCACAAG CCGTGGAGCA TGTGGTTTAA TTCGATGCAA 960
 CGCGAAGAAC CTTACCTGGT CTTGACATCC ACGGAAGTTT TCAGAGATGA GAATGTGCCT 1020
 55 TCGGGAACCG TGAGACAGGT GCTGCATGGC TGTCGTCAGC TCGTGTGTG AAATGTTGGG 1080
 TTAAGTCCCG CAACGAGCGC AACCTTATC CTTTGTGTC AGCGGTCCGG CCGGGAACCTC 1140
 60 AAAGGAGACT GCCAGTGATA AACTGGAGGA AGGTGGGGAT GACGTCAAGT CATCATGGCC 1200
 CTTACGACCA GGGCTACACA CGTGCTACAA TGGCGCATAA AAAGAGAAGC GACCTCGCGA 1260
 65 GAGCAAGCGG ACCTCATAAA GTGCGTCCGT AGTCCGGATT GGAGTCTGCA ACTCGACTCC 1320

	ATGAAGTCGG AATCGCTAGT AATCGTGGAT CAGAATGCCA CGGTGAATAC GTTCCCGGGC	1380
	CTTGACACACA CCGCCCGTCA CACCATGGGA GTGGGTTGCA AAAGAAGTAG GTAGCTTAAC	1440
5	CTTCGGGAGG GCGCTTACCA CTTTGTGATT CATGACTGGG GTGAAGTCGT AACAAGGTAA	1500
	CCGTA	1505

10 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20	AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA	60
	GTGCAACGGT AACAGGAAGA AGCTTGCTCT TTGCTGACGA GTGGCGGACG GGTGAGTAAT	120
	GTCTGGGAAA CTGCCTGATG GAGGGGGATA ACTACTGGAA ACGGTAGCTA ATACCGCATA	180
25	ACGTCGCAAG ACCAAAGAGG GGGACCTTCG GGCCTCTTGC CATCGGATGT GCCCAGATGG	240
	GATTAGCTAG TAGGTGGGGT AACGGCTCAC CTAGGCGACG ATCCCTAGCT GGTCTGAGAG	300
30	GATGACCAGC CACACTGGAA CTGAGACACG GTCCAGACTC CTACGGGAGG CAGCAGTGGG	360
	GAATATTGCA CAATGGGCGC AAGCCTGATG CAGCCATGCC GCGTGTATGA AGAAGGCCTT	420
	CGGGTTGTAA AGTACTTTCA GCGGGGAGGA AGGGAGTAAA GTTAATACCT TTGCTCATTG	480
35	ACGTTACCCG CAGAAGAAGC ACCGGCTAAC TCCGTGCCAG CAGCCGCGGT AATACGGAGG	540
	GTGCAAGCGT TAATCGGAAT TACTGGGCGT AAAGCGCACG CAGGCGGTTT GTTAAGTCAG	600
40	ATGTGAAATC CCCGGGCTCA ACCTGGGAAC TGCATCTGAT ACTGGCAAGC TTGAGTCTCG	660
	TAGAGGGGGG TAGAATTCCA GGTGTAGCGG TGAAATGCGT AGAGATCTGG AGGAATACCG	720
45	GTGGCGAAGG CGGCCCCCTG GACGAAGACT GACGCTCAGG TGCGAAAGCG TGGGGAGCAA	780
	ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG TCGACTTGGA GGTGTGCCCC	840
	TTGAGGCGTG GCTTCCGGAG CTAACGCGTT AAGTCGACCG CCTGGGGAGT ACGGCCGCAA	900
50	GGTTAAAACT CAAATGAATT GACGGGGGCC CGCACAAAGC GTGGAGCATG TGGTTTAATT	960
	CGATGCAACG CGAAGAACCT TACCTGGTCT TGACATCCAC GGAAGTTTTC AGAGATGAGA	1020
55	ATGTGCCTTC GGAACCGTG AGACAGGTGC TGCATGGCTG TCGTCAGCTC GTGTTGTGAA	1080
	ATGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTATCCT TTGTTGCCAG CCGTCCGGCC	1140
	GGGAACTCAA AGGAGACTGC CAGTGATAAA CTGGAGGAAG GTGGGGATGA CGTCAAGTCA	1200
60	TCATGGCCCT TACGACCAGG GCTACACACG TGCTACAATG GCGCATACAA AGAGAAGCGA	1260
	CCTCGCGAGA GCAAGCGGAC CTCATAAAGT GCGTCGTAGT CCGGATTGGA GTCTGCAACT	1320
65	CGACTCCATG AAGTCGGAAT CGCTAGTAAT CGTGGATCAG AATGCCACGG TGAATACGTT	1380

CCCCGGGCCTT GTACACACCG CCCGTCACAC CATGGGAGTG GGTGCAAAA GAAGTAGGTA 1440
 GCTTAACCTT CGGGAGGGCG CTTACCACTT TGTGATTCAT GACTGGGGTG AAGTCGTAAC 1500
 5 AAGGTAACCG TAGGGGAACC TGCGGTTGGA TCACCTCCTT A 1541

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACAGGAAGA AGCTTGCTCT TTGCTGACGA 30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AACAGGAAGC AGCTTGCTGT TTCGCTGACG A 31

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACAGGAAAC AGCTTGCTGT TTCGCTGACG A 31

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AACAGAAAGC AGCTTGCTCT TTGCTGACGA 30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 AACAGGAAGC AGCTTGCTCT TCGCTGACGA 30

(2) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGCAACG CGAAGAACCT TACCTGGTCT T 31

20 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

30 CGACGCAACG CGAAGAACTT ACCTGGTCTT 30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

45 GGAAGTTTT C AGAGATGAGA ATGTGCCTTC GGAACCGTG 40

(2) INFORMATION FOR SEQ ID NO:16:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGAAGTTTCC AGAGATGGAT TGGTGCCTTC GGAAGCTGTG 40

60 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
65 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 AGAAGCTTCC AGAGATGGAT TGGTGCCTTC GGGAACTGTG 40

(2) INFORMATION FOR SEQ ID NO:18:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGCTTGCTC TTCGCTGACG 20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

30 AAAGCAGCTT GCTCTTTGCT 20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

45 CGACGCAACG CGAAGAACTT 20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

60 GAAGCTTGCT TCTTTGCTGA C 21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
65 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGACGCAACG CGAAGAA

17

09027439 02200